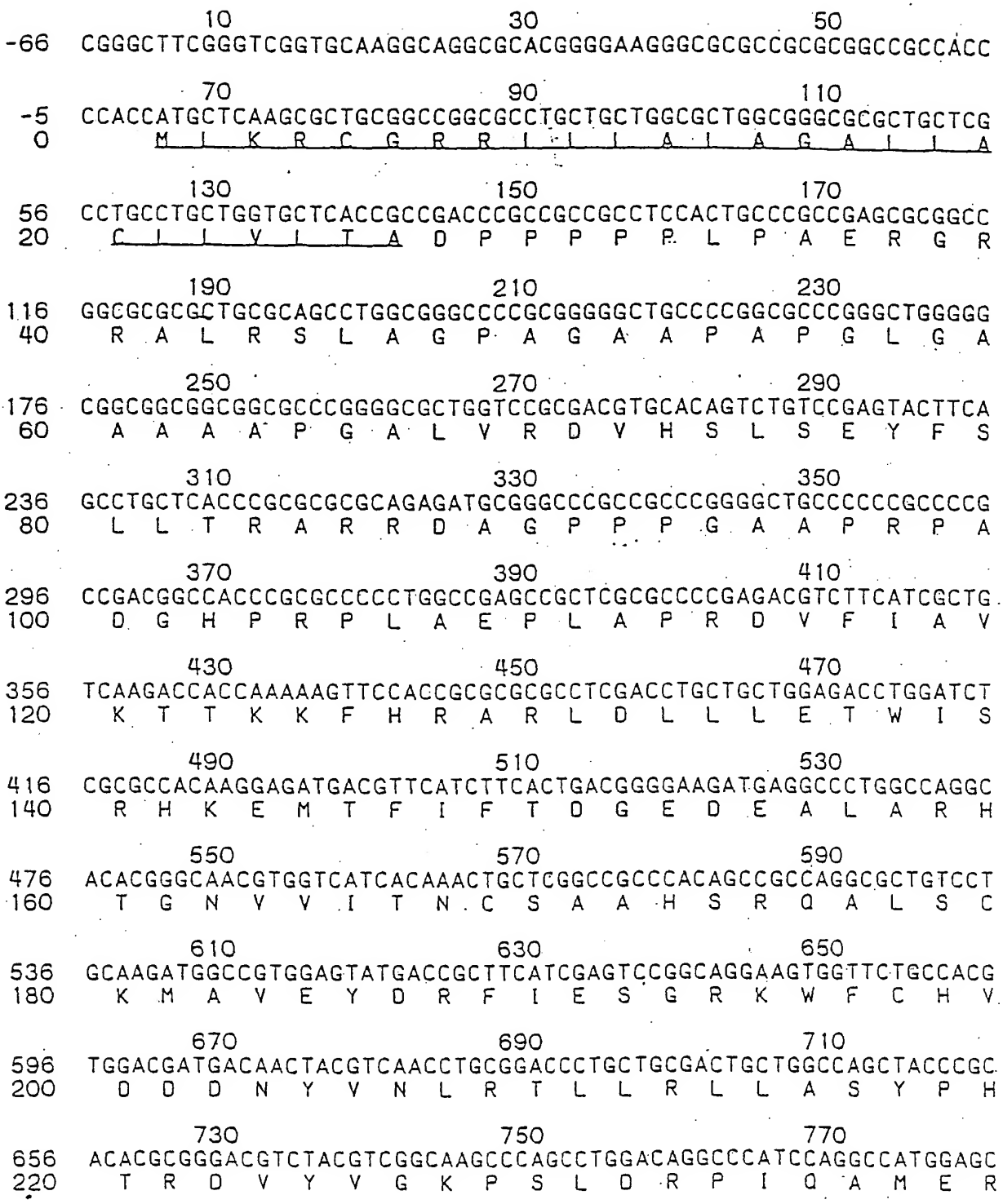
Figure 1A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70 90 110
-5 CCACCATGCTCAAGCGCTGCGGCCGGCGCCTGCTGCTGGCGCTGGCGGGCGCGCTGCTCG
0 M I K R C G R R I I I A I A G A I I A
130 150 170
56 CCTGCCTGCTGGTGCTCACCGCCGACCCGCCGCCGCCTCCACTGCCCGCCGAGCGCGGCC
20 C I I V I T A D P P P P P P L P A E R G R
190 210 230
116 GGCGCGCGCTGCGCAGCCTGGCGGGCCCCGCGGGGGCTGCCCCGGCGCCCGGGCTGGGGG
40 R A L R S L A G P A G A A P A P G L G A
250 270 290
176 CGGCGGCGGCGGCGCCCGGGGCGCTGGTCCGCGACGTGCACAGTCTGTCCGAGTACTTCA
60 A A A A P G A L V R D V H S L S E Y F S
310 330 350
236 GCCTGCTCACCCGCGCGCGCAGAGATGCGGGCCCGCCGCCCGGGGCTGCCCCCCGCCCCG
80 L L T R A R R D A G P P P G A A P R P A
370 390 410
296 CCGACGGCCACCCGCGCCCCCTGGCCGAGCCGCTCGCGCCCCGAGACGTCTTCATCGCTG
100 D G H P R P L A E P L A P R D V F I A V
430 450 470
356 TCAAGACCACCAAAAAGTTCCACCGCGCGCGCCTCGACCTGCTGCTGGAGACCTGGATCT
120 K T T K K F H R A R L D L L L E T W I S
490 510 530
416 CGCGCCACAAGGAGATGACGTTCATCTTCACTGACGGGGAAGATGAGGCCCTGGCCAGGC
140 R H K E M T F I F T D G E D E A L A R H
550 570 590
476 ACACGGGCAACGTGGTCATCACAAACTGCTCGGCCGCCCACAGCCGCCAGGCGCTGTCCT
160 T G N V V I T N C S A A H S R Q A L S C
610 630 650
536 GCAAGATGGCCGTGGAGTATGACCGCTTCATCGAGTCCGGCAGGAAGTGGTTCTGCCACG
180 K M A V E Y D R F I E S G R K W F C H V
670 690 710
596 TGGACGATGACAACTACGTCAACCTGCGGACCCTGCTGCGACTGCTGGCCAGCTACCCGC
200 D D D N Y V N L R T L L R L L A S Y P H
730 750 770
656 ACACGCGGGACGTCTACGTCGGCAAGCCCAGCCTGGACAGGCCCATCCAGGCCATGGAGC
220 T R D V Y V G K P S L D R P I Q A M E R

Figure 1B

```
          790                       810                       830
716  GGGTCAGCGAGAACAAGGTGCGTCCTGTCCACTTCTGGTTTGCCACGGGCGGCGCTGGCT
240    V  S  E  N  K  V  R  P  V  H  F  W  F  A  T  G  G  A  G  F

          850                       870                       890
776  TCTGCATCAGCCGTGGGCTGGCTCTGAAGATGAGCCCGTGGGCCAGCGGGGGTCACTTCA
260    C  I  S  R  G  L  A  L  K  M  S  P  W  A  S  G  G  H  F  M

          910                       930                       950
836  TGAATACGGCTGAGCGGATCCGGCTGCCTGATGACTGCACCATCGGCTACATCGTGGAGG
280    N  T  A  E  R  I  R  L  P  D  D  C  T  I  G  Y  I  V  E  A

          970                       990                      1010
896  CCCTGCTGGGTGTGCCCCTCATCCGCAGCGGCCTCTTCCACTCCCACCTGGAGAACCTGC
300    L  L  G  V  P  L  I  R  S  G  L  F  H  S  H  L  E  N  L  Q

         1030                      1050                      1070
956  AGCAGGTGCCCACCTCGGAGCTCCACGAGCAGGTGACGCTGAGCTACGGTATGTTTGAAA
320    Q  V  P  T  S  E  L  H  E  Q  V  T  L  S  Y  G  M  F  E  N

         1090                      1110                      1130
1016 ACAAGCGGAACGCCGTCCACGTGAAGGGGCCCTTCTCGGTGGAGGCCGACCCATCCAGGT
340    K  R  N  A  V  H  V  K  G  P  F  S  V  E  A  D  P  S  R  F

         1150                      1170                      1190
1076 TCCGCTCCATCCACTGCCACCTGTACCCGGACACACCCTGGTGTCCCCGCACTGCCATCT
360    R  S  I  H  C  H  L  Y  P  D  T  P  W  C  P  R  T  A  I  F

         1210                      1230                      1250
1136 TCTAGTGGCCATGGCTGAGACCCAATCCCTGGGCGCCCCTGGTATCCAAAGGGCCCAGGG

         1270                      1290                      1310
1196 ACCCTGTTGCGCTGCCCTGGCCTCGGCATTCGAGGCTCCCCTAGGGCCGTGCCTGTGCGT

         1330                      1350                      1370
1256 GTGCGTGTGCGTGTGTGTGTGTGTACTGCATGCCCACCCGGGTAGCAGGCTGCTGGGC

         1390                      1410                      1430
1316 AGTTCTGCTCTGTGGAGGGGCGGGCACCAGCGCCACTTATGTGCCTCTGCTCCGAGGGCC

         1450                      1470                      1490
1376 AGTGGTATGGAGGGTCTGCTTGGAGGAAGGATTTGTGTGTCGGAGGACACTCCGAGGGCA

         1510                      1530
1436 ATTCTGTTAGGATTTGTGGATCTTTCTACAGCTACGGGGCTCCGG
```

Figure 2


1 MLKRCGRRLLLALAGALLACLLVLTADPPPPPLPAERGRRALRSLAG.PA 49
1 MLKNWGKKLLLSIVGATLTCLLVLVVDQQSRHMLETQSDHEPGSAAAVHL- 50
50 GAAPAPGLGAAAAAPGALVRDVHSLSEYFSLLTRARRDAGPPPGAAPRPA 99
51 RADLDPANPGDGGDPANSAQDSGTFSAYFNKLTRVRRDVEQVAAPSKDSA 100
100 DGHPRPLAEPLAPRDVFIAVKTTKKFHRARLDLLLETWISRHKEMTFIFT 149
101 APE.....EDITANDVFIAVKTTKKFHRSRMDLLMDTWISRNKEQTFIFT 145
150 DGEDEALARHTGNVVITNCSAAHSRQALSCKMAVEYDRFIESGRKWFCHV 199
146 DGEDEELQKKTGNVESTNCSAAHSRQALSCKMAVEYDKFIESDKKWFCHV 195
200 DDDNYVNLRTLLRLLASYPHTRDVYVGKPSLDRPIQAMERVSENKVRPVH 249
196 DDDNYVNVRTLVKLLSRYSHTNDIYIGKPSLDRPIQATERISESNMRPVN 245
250 FWFATGGAGFCISRGLALKMSPWASGGHFMNTAERIRLPDDCTIGYIVEA 299
246 FWFATGGAGFCISRGLALKMSPWASGGHFMNTAEKIRLPDDCTIGYIIES 295
300 LLGVPLIRSGLFHSHLENLQQVPTSELHEQVTLSYGMFENKRNAVHVKGP 349
296 VLGVKLIRSNLFHSHLENLHQVPQSEIHNQVTLSYGMFENKRNAILMKGA 345
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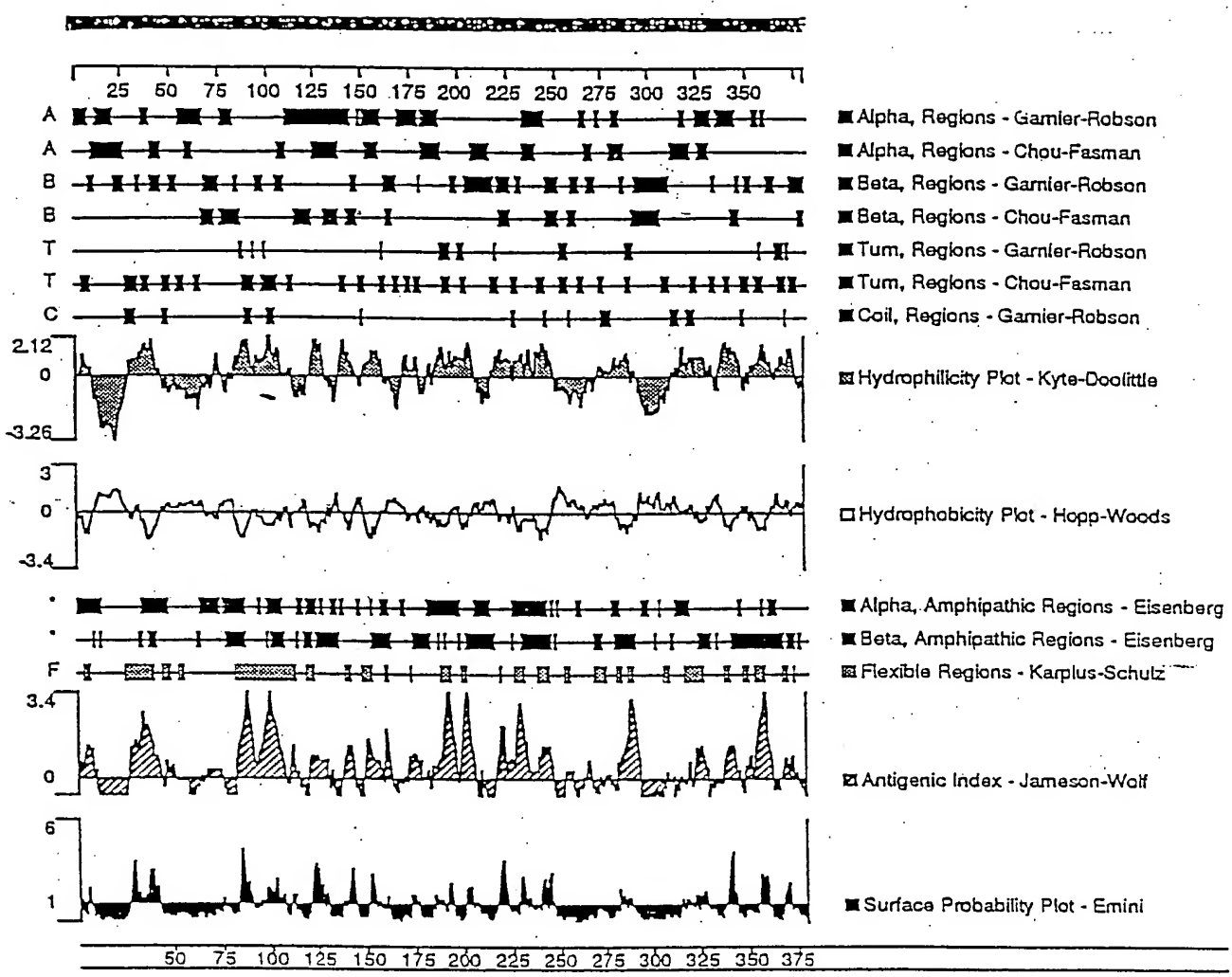
346 FSVEEDPSRFRSVHCLLYPDTPWCPWKAAY 375

Figure 3


25 50 75 100 125 150 175 200 225 250 275 300 325 350
A
A
B
B
T
T
C
Alpha, Regions - Garnier-Robson
Alpha, Regions - Chou-Fasman
Beta, Regions - Garnier-Robson
Beta, Regions - Chou-Fasman
Turn, Regions - Garnier-Robson
Turn, Regions - Chou-Fasman
Coil, Regions - Garnier-Robson
2.12
0
-3.26
Hydrophilicity Plot - Kyte-Doolittle
3
0
-3.4
Hydrophobicity Plot - Hopp-Woods
Alpha, Amphipathic Regions - Eisenberg
Beta, Amphipathic Regions - Eisenberg
F
Flexible Regions - Karplus-Schulz
3.4
0
Antigenic Index - Jameson-Wolf
6
1
Surface Probability Plot - Emini
50 75 100 125 150 175 200 225 250 275 300 325 350 375